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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Match
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1: pir1:*
2: pir2:*
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Copyright (c) 1993 - 2000 Comp
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B75556
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412 V-FRNTLLETRPSSRRLELPMPPADFGQTVANNPKIEQSLLKETLGCYLVHSKMRNPVFQ

470 405

TTTNEWNGFANPDDVVTFGQ------TGGAAGTNATITITAPTVTLTILATTTSAANV PNDGSWTDFASAGDTVTFRQVAVDEVVVTNNPAGGG-----SAPTFTVRV-PPSNAYTNT 411

354

358 295 298

235 CSDYRLTYKSITCEANMPTLVDQGFWIGGHYALTPIATTQNAVEGSGFEHPFNVTRPGIA

VSDYRLTYKAITCEANMPTLVDQGFWIGGQYALTPTSLPQYDVSEAYALHTLTFARPSSA

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. 297 294

238

Db Qy	Оу	Дb	Quer Best Matc	RESULT A43370 capsid C;Spec C;Date C;Date C;Agra Virolo A;Til A;Refie A;Acce A;Role A;Resi A;Cros C;Supe		***
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			Query Match Best Local Similarity Matches 425; Conser	RESULT 1 A4370 capsid protein - Nudaurelia o capsid proteis: Nudaurelia omega v C;Species: Nudaurelia omega v C;Date: 16-Jul-1999 #sequence C;Accession: A4370 C;Accession: A4370 R;Aqrawal, D.K.; Johnson, J.E Virology 190, 806-814, 1992 A;Title: Sequence and analysi A;Reference number: A4370; M A;Accession: A4370 A;Accession: A4370 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-644 <agr>A;Cross-references: GB:S43937 C;Superfamily: Nudaurelia ome</agr>		113 112.5 111.5 111.5 111.5 111.5 111.5 110.5 1109.5 1109.5 1109.5 109.5 109.5 109.5 109.5
	TYTEPANI	SQRPHNRRGTRNVRV : : : snsasgkrrsrnvriar	64. Llarity 64. Conservative	Nudaure :elia om j99 #seq 370 Johnson 5-814, 1 5-814, 1 7		
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ECPS	FRM : FRSI	RGRR	7 de de ;	mega irus rev Trev ga v		000000000000000000
DASIPLDGAQWSLSII EQWINETNDTTYYVRI :: :: :: ::	QSLDANTVTFPANISSMPEFRNWAKGKIDLDSDSIGWYFKYLDPAGATESARAVGEYSKI : ::: : :	AR	Score 2179; DB 2; Pred. No. 2e-145; 68; Mismatches 130;	RESULT 1 A43370 C; Species: Nudaurelia omega virus C; Accession: A43370 R; Aqrawal, D. K.; Johnson, J.E. Virology 190, 806-814, 1992 Virology 190, 806-814, 1992 A; Title: Sequence and analysis of the capsid protein A; Fitle: Sequence and analysis of the capsid protein A; Reference number: A43370; MUID:92391097 A; Accession: A43370 A; Status: preliminary A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-644 <agr> A; Cross-references: GB:643937 A; Cross-references: GB:643937</agr>	ALIGNMENTS	E71086 E71086 S59077 AD1512 T31042 T31042 T5563 E75563 E75563 E7563 E
:		SANTYTYNGRRNGRRTGROVSPDDNFTAAAQDLA 57 : SANTYNVAPKQRANNIDNYTAAAQELG 54	Length 644; ; Indels 34; Gaps 7;	RESULT 1 A43370 C;Date: Nudaurelia omega virus C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999 C;Accession: A43370 C;Accession: A4370 N;Aqrawal, D.K.; Johnson, J.E. Virology 190, 806-814, 1992 A;Mitle: Sequence and analysis of the capsid protein of Nudaurelia capensis omega vir A;Reference number: A43370 A;Reference number: A43370 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-644 <agr> A;Cross-references: GB:S43937 A;Cross-references: GB:S43937</agr>		hypothetical prote hypothetical prote cellulose 1,4-beta peptidoglycan boun hypothetical prote lactocepin (EC 3.4 endoglucanase - Er probable peptidyl-protein F56b6.1 [i mofA protein precu flagellar hook pro CT711 hypothetical conserved hypothet multidrug resistan laminarinase - The hypothetical protein protein protein resistan laminarinase - The hypothetical protein multidrug resistan laminarinase - The

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INFRNLDAETTAASNRSEVPLPPLTFGQTAPNNPKIEQTLVKDTLGSYLVHSKMRNPVFQ

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C;Accession: B75556
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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B75561
C:Species: Deinococcus radiodurans (strain C:Species: Deinococcus radiodurans C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ter
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A;Molecule type: APII>
A;Res1dues: 1-597 <WHI>
A;Cross-references: GB:AE001876; GB:AE000513; NID:g6457800; PIDN:AAF09732.1; PID:g645780
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  YASVGGGGDPDVLPTPGATCTGEQCASDPTTV
                                                                                                                                                                                                                                                                                          TLVDQG----FWIGGQYA------LTPTSLPQYDVSEAYA-------LHTLTFARPSSA
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                                        LLETRPSSRRLELPMPPAD-FGQTVANNPKIEQSLLKETLGCYLVHSKMRNPVFQLT---
                                                                                 TTAGGSFGTRPASGAT - - - - - GRVDWTFTPSTPLAAGQSLTFTVTVNVANTVANGATLTN
                                                                                                                        PN-DGSWTDFASAGDTVTFRQVAVDEVVVTNNPAGGGSAPTFTVRVPPSNAYTNTVFRNT
                                                                                                                                                                                                          AALAFVWAGLPQGGTAPAGTPAWEQASSGGYLTWRHNGTTFPAGSVSYVLPEGFALERYD
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T.; Zalewski,
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: S09843; S51034; S51035
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Home, Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Note: assembly protein release site (Ala-256--Ser-257) and C:Superfamily: cytomegalovirus capsid assembly protein C:Keywords: capsid assembly; hydrolase; serine proteinase F:1-256/Product: viral proteinase #status predicted <PMAT> F:336-708/Product: capsid assembly protein #status predicted F:132/Active site: Ser #status experimental #status ef:643-644/Cleavage site: Ala-Ser (viral proteinase) #status ef:643-644/Cleavage site: Ala-Ser (viral proteinase)
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A; Note: the DNA sequence was submitted to EMBL, December 1989, in computer-readable R; Stevens, J.T.; Mapelli, C.; Tsao, J.; Hall, M.; O'Boyle II, D.; Weinheimer, S.P.; Eur. J. Biochem. 226, 361-367, 1994
A; Title: In vitro proteolytic activity and active-site identification of the human cap; Reference number: S51034; MUID:95094793
A; Accession: S51034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UL80 protein - human cytomegalovirus (strain AD169)
N;Contains: capsid assembly protein; viral proteinase
C;Species: human cytomegalovirus, human herpesvirus 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 110-131, 'X', 133-134 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Curr Top. Microbiol. Immunol. 154, 125-169, 1990 A;Title: Analysis of the protein-coding content of A;Reference number: S09749; MUID: 90269039 A;Accession: S09843
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A; Residues: 1-708 <CHE>
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                     496
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                                                                                                                                                                                                                                                                                                                                                      269 ALTPTSLPQYDVSEAYAL-HTLTFARPSSAAALAFVWAGLPQGGTAPAGTPAWEQASSGG 327
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                    YLTWRHNGTTFPAGSVSYVLPEGFALERYDPNDGSWTDFASAGDTVTFRQVAVDEVVVTN 387
                                                            LAARHFADYVDPHYPGWGRRYEPAPSLHPSYPVPPPPS-----PAYYRRRDSPGGMD
                                                                                                                                                                                                                                                                                                                AESPPSLSPSEPAEAASMSHPLSAAVPAATA-----PPGATVAGASPA---VSS-- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMSFTLTPQAGDIITCSVGD
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                                                                                                                                                                                     NPAGGGSAPTFTVRVPPSNAYTNTVFRNTLLETRPSSRRLELPMP--PADFGQTVANNPK
                                                                                                                                                                                                                                -LAWPHDGVYLPKDAFFSLL-------
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                                                                                                                                            -GASRSAVPVMYPGAVA
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                     YTGIRDSFDQNM
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                                                                                                   -GCYLVHSKMRNPVFQLTPASSFGAVSFNNPGYERTRDLPD---
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                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 130; DB Pred. No. 0.46;
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                                                                                                                                            -APPSASPAPLPLPSYPASYGAPVVGYDQ
-STAVAHFRSLSHSCSIVTKTYQGWEG
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                                                                                                                                                                                                                                                                                                                                                                                               151;
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C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45025
R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Biol. Chem. 272, 318-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various alternat A;Reference number: 222899; MUID:97166151
A;Reference number: 222899; MUID:97166151
proteinase related protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change
                                                                    RESULT
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A;Cross-references: EMBL:272496; NID:91834502; PIDN:CAA96577.1;
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Best Local :
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                                                                                                                                                                                                  603 SV 604
                                                                                                                                                                                                                                           923 STPALSSPHPSSRTTESPPSPGTTTPGHTTATSRTTATATPSKTRTSTLLPSQPTSAPIT 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSGGYLTWRHNGTTFPAGSVSYVLPEGFALERYDPNDGSWTDFASAGDTVTFRQVAVDE 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPPSGWERYDGGHRGQSQKQHRHGGSGGHNKRRKETAAASSSSSDEDLSFPGEAEHGRAR
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Pred. No. 11;
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  24-May-2001 #text_change 24-May-2001
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A; Reference number: Z20512
A; Accession: T28698
A; Status: preliminary; translated
                                                                       R;Parkhill, J.; Bentley, S. submitted to the EMBL Data A;Reference number: Z20512
                                                                                                          hypothetical protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T28698 R; Parkhill, J.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
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A; Residues: 1-1269 <KUR>
A; Cross-references: GB:AE006641;
C; Genetics:
A; Gene: SSO1141
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A;Accession: A90267
A;Status: preliminary
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Red
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolopus solfataricus complete genome.
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A; Molecule type: DNA
A; Residues: 1-2314 < PAR>
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Best Local S
Matches 98
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19.6%; Pred. No. 2.4;
tive 69; Mismatches
                                                                                       .D.; Barrell, B.G.; Rajandream,
Library, January 1999
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Redder
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EMBL: AL023496; NID: e1292348; PID: e1292365; PIDN: CAA18915.1

C;Genetics: A;Gene: PAB1 C;Keywords:

PAB1252

hydrolase

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1204 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960;
A;Experimental source: strain Orsay
                                                                                                                                                     probable pyrolysin (EC 3.4.-.-) homolog PAB1252 [similarity] - C;Specles: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change C;Accession: C75015 R;anonymous, Genoscope
                                                                                     submitted to the EMBL Data Library, July 1999 A;Description: Pyrcoccus abyssi genome sequen A;Reference number: A75001 A;Accession: C75015
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EGTYEVKVPVVNN---APAIFVNSTAIEDVVKGKANATLVAGWNVTVTTKTEVG
                            -GVY----PATDNFAAAVSAFA-ANMLSSVLKSEATSSIIKSVGETAVGAAQSG
                                                              ARVHF-VVSANAKVTPVTVEN----TTVT-----VGVTGNATITVTNDTVVANVTTS
                                                                                          AVAHFRSLSHSCSIVTKTYQGWEGVTNVNTPFGQFAHAGLLKNEEILCLADDLATRLT--
                                                                                                                                               LGCYLVHSKMRNPVFQLTPASSFGAVSFNNPGY---ERTRDLPDYTGIRDSFDQ--NMST
                                                                                                                                                                                                               TNTVFRNTLLETRPSSRRLELP-------MPPADFGQTVANNPKIE-QSLLKET
                                                                                                                                                                                                                                                                              DFASAGDTVTFR----QVAVDEVVVTNNP---AGGGSAPT-----FTVRVPPSNAY
                                                                                                                                                                                                                                                                                                                                                                        DFWMDYISDKELSIIKQNVNEIESILPQAHPFPDSPMAFDVSEAIDYIMWEILESNITPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQKINATFYTRFVNNETWWEEASFYLSTYSLRGEEW--FVNNAFVDIYALLNFMWMLYYI 458
                                                                                                                          LKITNVTAEVGGKSIELT----YNATS----GYYTGKVTLENGAYTLVVTATDELNNVGT
                                                                                                                                                                                    SAGTYNYTVVVTYPNGKEVALPSRIVTISGPTIKIVSPVD---TVYNVTTIPIEVLVNHT
                                                                                                                                                                                                                                               SYDKAPNNVTIKYGDENVSIYSIIPLEGAKVVIGGKEYPLKAEEGGYYYYGTEIAEKLEL
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145; Conserv
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RESULT 8
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#text_change

26-Aug-1999

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submitted to the EMBL Data Library, October 1992
A; Description: Sequences of the membrane proteins gp 350/220 a
A; Reference number: S29605
A; Raccession: S29605
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-886 < KLE>
A; Cross-references: EMBL:X67776; NID:g59163; PIDN:CAA47986.1;
C; Superfamily: Epstein-Barr virus membrane antigen gp350
C; Keywords: glycoprotein
RESULT 9
AC1153
adhesin homolog lmo0627 [imported] - Listeria monocytogenes (str C:Species: Listeria monocytogenes (c;Species: Listeria monocytogenes (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change C:Accession: AC1153
R:Glaser, P:; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, :; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.;
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      Berche, P.;
tian, K.D.;
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1153
A;Cession: AC1153
membrane antigen gp350 - human herpesvirus 4 (strain C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequenevision 25-Feb-1985 #t C;Accession: A43042; S33008; S33009; A03762 R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barr Mol. Biol. Med. 1, 21-45, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1582 <GLA>
A; Cross references: GB:NC_003210; PIDN:CAC98705.1;
A; Experimental source: strain EGD-e
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122; Conserv
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92; Mismatches
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Voss, H.; W
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A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome A;Reference number: A03794; MUID:84270667
A;Contents: annotation; protein coding region C;Superfamily: Epstein-Barr virus membrane antigen gp350
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A;Molecule type: DNA
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A; Residues: 1-907 <FA2>
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A; Accession: S33008
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A; Residues: 1-907 <BAN>
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                                                                                                                                                                                                                                                               TGPTVSTADVTSPTPAGTTSGASP---
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 HSCSIVTKTYQGWEGVTNVNTPFGQFAHAGLLKNEEILCLADDLATRLTGVYPAT----
                                                                                                             TSPTSAVTTPTPNATSPTLGKTSPTS-AVTTPTPNAT-GPTVGETSP-QANATNHTLG--
                                                                                                                                                                                        TPNATSPTPAVTTPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSPTLGK
                                                                                                                                                                                                                            TFRQVAVDEVVVT - - - - -
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                                        ---GTSPTPVVTSQPKNATSAVTTGQ--HNITSSSTSSMSLRPSSNPETLSPSTSDNSTS
                                                                         LVHSKMRNPVFQLTPASSFGAVSFNNPGYERTRDLPDYTGIRDSFDQNMSTAVAHFRSLS
                                                                                                                                                                                                                                                                                                  SGGYLTWRHNGTTFPAGSVSYVLPEGFALERYDPNDGSW------TDFASAGDTV
                                                                                                                                                                                                                                                                                                                                                                                                             AWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDITVSGLGTAPKTLIITRTATNA
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                                                                                                                                                                                                                                                                                                                                                                       -SLPQYDVSEAYALHTLTFARPSSAAALAFVWAGLPQGGTAPAGTPAWEQAS
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19.6%; Pred. No. 2.
                                                                                                                                                -TLLETRPSSRRLELPMPPADFGQTVANNPKIEQSLLKETLGCY
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C;Accession: B75514
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Cross-references:
C;Genetics:
                                            A; Molecule type: mRNA
A; Residues: 1-889 <JIN>
                                                                                                        A; Reference number: A; Accession: T09055
                                                                                                                            R; Jin, P.; Xu, H.; Israel, submitted to the EMBL Data A; Reference number: 216540
                                                                                                                                                                                          protocadherin 68 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09055
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Best Local Similarity
Thes 72; Conserve
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A;Gene: DR0479
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A; Residues: 1-873 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              penicillin-binding protein 1 - Deinococcus radiodurans (strain
C; Species: Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain
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                                                                                    Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                    757 LPRQTSPRRALPS----RTCRPRRPLSPPPRRPRPGA 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GGLATRARI-----DGWQVGGKTGTT-----NDVKD-----LWFAGVTPLTSGA--
                                                                                                                                                                                                                                                                                                                                                                                                            FTVRVPPSNAYTNTVFRNTLLETRPSSRRLELPMPPA 434
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                        EMBL:AF029343; NID:g2599501; PID:g2599502
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26.0%;
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Library, October 1997
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Pred. No. 3
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T.; Zalewski,
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: F90073 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-2271 <KUR>
A;Cross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                              C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, Lancet 357, 1225-1240, 2001
A:Title Whole A: Title Whole A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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C; Genetics:
A; Gene: SA2
                       A; Experimental source: strain N315 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                   R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRHNGTTFPAGSVSYVLPEGFALERYDPNDGSWTDFASAGDTVTFRQV---AVDEVVVTN 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDSEQWINFTN-----DTTY----YVRIRVLRPTYDVPDPTEGLVRTVS--DY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T----ALDGGE------PPRSATVQINVKVIDSNDNSPVFEAPSYLVELPENTPLGTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDVSVPLDGRQWSLSIFSFPMFRTAYVAVANVENKEMS--LDVVNDLIEWLNNLADWRYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-----APPGTVIALVRVTDRDSGKNGQLQCRVLGGGGTGGGG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GLGGPGGSVPFKLEENY------DNFYT------VVTDRPMDRETQDEYNVTI
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Pred. No. 3.6;
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Sekimizu,
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	SASLSDSTSNAISTSTSLS
	556 LCLADDLATRLTGVYPATDNFAAAVSAFAANMLSSVLKSBATSSIIKSVGETA 6
555 876	Qy 508 STAVAHFRSLSHSCS-IVTKTYQGWEGVTNVNTPFGQFAHAGILKNEEI
507 825	Qy 449 SILKETIGCYLVHSKMRNPVFQLTPASSFGAVSEN-NPGYERTRDLPDYTGIRDSFDQNM
448 777	Qy 409 TNT
408 724	Qy 359NDGSWTDFASAGDTVTFRQVAVDEVVVTNNPAGGGSAPTFTVRVPPSNAY
358 685	Qy 318 PAWEQASSGGYLTWRHNGTTFPAGSVSYVLPEG-FALERYDP
317 630	Qy 264 IGGQYALTPTSLPQYDVSEAYALHTLTFARPSSAAALAFVWAGLPQGGTAPAGT
263 587	Qy 205 WINFTN-DTTYYVRIRVLRFTYDVPDPTEGLVRTVSDYRLTYKAITCEANMPTLVDQGFW
204 536	Qy 163FRT-AYVAVANVENKEMSLDVVNDLIEWLNNLADWRYVVDSEQ
162 476	Qy 127PAEIREIYNEECPVVTDVSVPLDGRQWSLSIFSFPM
126 421	Qy 98YLDPAGATESARAVGEYSKI
97 361	Qy 71 ISSMPEFRNWAKGKIDLDSDSIGWYFK
70 303	Qy 22 VSANTYTVNGRRNQRRRTGRQVSDPDNFTAAAQDLAQSLDANTYTFPAN 70
βĠ	Query Match 3.5%; Score 119.5; DB 2; Length 2271; Best Local Similarity 18.9%; Pred. No. 15; Matches 147; Conservative 107; Mismatches 233; Indels 289; Gaps

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ULT 14
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743220
743220
radin-like growth factor-l receptor - common lancelet
N,Alternate names: insulin-like peptide receptor
C;Species: Branchiostoma lanceolatum (common lancelet)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: 743220
R;Pashmforoush, M.; Chan, S.J.; Steiner, D.F.
Mol. Endocrinol. 10, 857-866, 1996
A;Title: Structure and expression of the insulin-like peptide receptor from amphioxus
A;Reference number: Z22346; MUID:96408719
A;Kotession: T43220
A;Kotession: T43220
A;Kotecule type: mRNA
A;Kolecule type: mRNA

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A; Nicessaudininary
A; Status; preliminary
A; Molecule type: DNA
A; Residues: 1-1993 <GLA>
A; Cross-references: GB: AL592022; PIDN: CAC95374.1;
A; Cross-references: Strain Clip11262
                                                                        A; Experimental source: strain C; Genetics: A; Gene: lin0141
                                                                                                                                                                                                                      Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                        probable peptidoglycan bound protein (LPXTG motif) lin0141 [imported] - Listeria C;Species: Listeria innocua C;Species: Prov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AF1450 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; F.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fs
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AF1450
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D.; Jones, L.M.; Karst, U.
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A;Residues: 1-1363 <PAS>
A;Cross-references: EMBL:S83394; NID:g1911771; PID:g1911772; PIDN:AAB50848.1
C:Superfamily: insulin receptor; protein kinase homology
C;Keywords: hormone receptor
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3.5%;
19.3%;
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19.8%; Pred. No. 7.6;
Live 60; Mismatches
Score
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EVVEGKVA
                                                                DNFVRAMSRDGSEIPMSKVKVEGKVN-TKKAGKYQVTYTIDPNEGTVDAGKEELSVTATI 1925
                                                                                               DNFAAAVSAFAANMLSSVLKSEATSSIIKSVGETAV----
                                                                                                                                GRVDNQTPGTYEITYR-YDGVTSVSRVTVLQNHAKIIVNDSKL-----KINADWDAK
                                                                                                                                                                FRSLSHSCSIVTKTYQGWEGVTNVNTPFGQFAHAGLLKNEEILCLADDLATRLTGVYPAT
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1933
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                                                                                                                                                                                                                                  ----RTRDLPDYTG----IRDSFDQ-----
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Search completed: May 29, 2002, 11:40:28 Job time: 100 sec